Role of cross-links in bundle formation, phase separation and gelation of long filaments

A. G. Zilman and S. A. Safran

Dept. of Material and Interfaces, Weizmann Institute of Science, 76100 Rehovot

Abstract. – We predict the thermodynamic and structural behavior of solutions of long cross-linked filaments. We find that at the mean field level, the entropy of self-assembled junctions induces an effective attraction between the filaments that can result in a phase separation into a connected network, in equilibrium with a dilute phase. A connected network can also be formed in a non-thermodynamic transition upon increase of the chain, or cross link density, or with decreasing temperature. For rigid rods, at low temperatures, we predict a transition from an isotropic network, to anisotropic bundles of rods tightly bound by cross links, that is triggered by the interplay between the configurational entropy of the cross-link distribution among the rods, and the rotational and translational entropy of the rods.

Introduction – Branched structures and networks are found in many physical, chemical and biological systems. Physical examples include gels, microemulsions/wormlike micelles, polymer-colloid dispersions and dipolar fluids [1–5, 15, 24–26]. Gelation and network formation have been studied in a number of experimental [4, 15, 24–27] and theoretical [7, 8, 12–14, 18, 19, 28] works and simulations [9, 11]. However, the connection between gelation and a first order phase separation that commonly accompanies the network formation, remain elusive [8–10]. Gels of rigid filaments such as actin cross-lnked with α- actinin [4], or charged polyelectrolytes such as DNA, cross-linked with multivalent ions, [21, 22] show a qualitatively similar thermodynamic behavior, and also have been shown to form compressed bundles of filaments, tightly bound by the cross-links. Their origin has been subject of recent theoretical activity [20, 31].

In this paper, we predict, at the mean field level, the phase diagram of a generic system of cross-linked equilibrium chains in terms of two independent transitions in the system. The first is a *continuous*, non thermodynamic, topological transition, where an infinite network spanning the entire volume of the system is formed. A second, entropically driven, first-order thermodynamic phase transition is predicted to occur even in the absence of any specific interactions. For most values of the control parameters, this latter transition is a sharp jump from a dilute solution of weakly branched chains to a connected dense network. The results, shown in Fig.1, predict the critical cross-link density and temperature for these transitions. In addition, we find that the entropy of the cross links can also drive a transition where

the system forms nematically aligned bundles of chains. The bundle transition, as well as the phase separation and gelation lines predicted, are consistent with the experiments on actin [4].

We study a generic model system that consists of identical monomers that self-assemble into chains, far above the polymerization transition, where the chains just start to form [6]. The chains, in turn, can branch in the presence of cross links. In order to elucidate the universal nature of our predictions, we assume *no specific interactions* between the monomers, except excluded volume, which means that the chains are self-avoiding and mutually avoiding. The system is characterized by the following parameters: the monomer density ϕ, the energies of the ends and junctions (branching points) ϵ_e and ϵ_j, measured relative to the energy of a bond between two monomers within the chain, the temperature T, the density of cross-links c, and the density of the capping molecules responsible for the formation of the ends, ρ. The numbers (per unit volume) of branching points, ϕ_j, and free ends, ϕ_e, are not fixed but are predicted as functions of ϕ, T, c and ρ. Here, we focus on the case of sparse junctions and ends, $\phi_j, \phi_e \ll \phi$. The complementary case of very dense junctions is better addressed using a different framework and is studied elsewhere [30].

This formulation allows us to pinpoint the difference between weak and strong cross-linking (i.e., physical gels vs. chemical gels) that correspond to positive and negative junction energies ϵ_j, respectively. In the case of strong cross links, the density of the cross links must be sufficiently low ($c \ll \phi$) so that the total number of junctions formed is small ($\phi_j < c \ll \phi$). Of course, in the case of strong cross-linking ($\epsilon_j < 0$), the experimental timescale at which true, equilibrium thermodynamic behavior is observed, strongly increases as ϵ_j decreases.

Theoretical Model: We begin by considering the system in the grand-canonical ensemble where the network is in equilibrium with a reservoir of *ends* and *junctions* of chemical potential μ_e and μ_j respectively. In this formulation the numbers of ends and junctions are not conserved but determined by the values of μ_e and μ_j, respectively; these are calculated below. Both junctions and ends can be viewed as "thermal defects" of the system whose "ground state" we consider to be an assembly of infinite linear chains. For flexible chains, in the random mixing approximation [2], the excluded volume part of the free energy is $\frac{1}{2}\phi^2$. For rigid rods, the angular average of the excluded volume interaction between the rods is $\frac{1}{2}vn^2$, with $v \simeq dL^2$, $n = \phi/L$, where d is the rod diameter (taken as unity in our lattice model) and L is the average length of the chains [16, 17]. The excluded volume interaction thus scales as $\frac{1}{2}\phi^2$ for both flexible chains and rigid rods.

General thermodynamic considerations (as well as rigorous treatments [29]) show that in the limit of a low density of non-interacting ends and junctions, every non-conserved, thermally generated junction or end lowers the free energy by $k_{\mathrm{B}}T$. At the mean field level of analysis, the grand-canonical potential of the system (per unit volume) is given by $\Omega(\phi, \mu_j, \mu_e, \epsilon_j, \epsilon_e) = \frac{1}{2}\phi^2 - \phi_e - \phi_j$ where ϕ_e and ϕ_j are the densities of ends and junctions. The physics of the problem lies in the dependence of ϕ_e and ϕ_j on the parameters of the system, such as the monomer density ϕ, temperature T and the chemical potentials μ_j and μ_e. It can be understood via a simple probabilistic argument: two ends are formed whenever a bond is broken by thermal fluctuations in the presence of two available end cap molecules. To the first order in the number of ends and junctions, the number of bonds is proportional to the number of the monomers, ϕ. Taking into account the free energy of formation of two ends, $2(\epsilon_e - \mu_e)$, the probability of bond breaking is $\phi e^{2(\mu_e - \epsilon_e)/T}$. In equilibrium, this must be equal to the probability of bond formation from the coalescence of two ends. In the random mixing approximation, the probability of a collision of two ends is $\phi_e^2 a_1^{-2}$ where the numerical prefactor a_1 reflects the microscopic properties of the ends, such as flexibility of the chains and effective collision cross-section. We thus find $\phi_e = a_1 e^{(\mu_e - \epsilon_e)/T}\phi^{1/2}$. Similarly, an f-fold junction can form through a collision of $f - 2$ ends and an internal monomer

(or a collision of f ends). The creation of $f - 2$ ends at the expense of a junction costs an energy $(f - 2)(\epsilon_e - \mu_e) - \epsilon_j + \mu_j + T \ln a_f$, where the coefficient a_f reflects the microscopic degrees of freedom of the junction, and includes the entropy of configurations of the bonds and monomers in the junction. The probability of junction break-up is thus equal to $\phi_j a_f{-1} e^{(-\mu_j + \epsilon_j)/T} e^{(f-2)(-\epsilon_e + \mu_e)/T}$. Equating this with the probability of collision of $f - 2$ ends with an internal monomer, $\phi_e^{f-2} \phi a_1^{2-f}$, we find for the junction and end densities

$$\phi_j = a_f e^{(\mu_j - \epsilon_j)/T} \phi^{f/2} \qquad \phi_e = a_1 e^{(\mu_e - \epsilon_e)/T} \phi^{1/2}$$

Therefore, in the random mixing approximation, the grand canonical potential of the system for the case of sparse junctions and ends $(\phi_j, \phi_e \ll \phi)$ is :

$$\Omega(\phi, \mu_j, \mu_e)/T = \frac{1}{2}\phi^2 - a_1 e^{(\mu_e - \epsilon_e)/T} \phi^{1/2} - a_f e^{(\mu_j - \epsilon_j)/T} \phi^{f/2} \tag{1}$$

Subsequently, we put $a_1 = 1$ for convenience. Equation (1) can also be derived rigorously [12, 28, 29] as described in [29], or, in some particular cases, by heuristic methods [11, 19, 32].

It is important to note that at this mean field level it is of no consequence whether in the absence of any junctions or ends (zero temperature) the "ground state" consists of infinite chains or closed rings. For strong cross-linking, the junctions persist at low temperatures and the number of closed linear rings is exponentially small compared with number of branched aggregates. Even for weak junctions, the number of closed rings relative to the number of chains is smaller by a factor $L^{-3/2}$ (where L is the chain length). Their influence is of importance only at extremely low temperatures and densities, Ref. [6, 18]. In addition, the role of intra-cluster loops [11] is outside the scope of our model, because the information about the long range correlations along a chain is lost in the mean field approximation.

We now proceed to transform the grand-canonical potential $\Omega(\phi, \mu_j)$ of Eq.(1) and express the free energy as a function of the physical cross link and end cap densities, c and ρ, respectively, instead of the chemical potentials μ_j and μ_e. The free energy of a system of branched chains in terms of the junction and ends densities ϕ_j and ϕ_e, is given by the Legendre transform of the free energy Eq. (1) $F(\phi, \phi_j, \phi_e) = \Omega(\phi, \mu_j, \mu_e) + \mu_j\phi_j + \mu_e\phi_e$:

$$F(\phi, \phi_j, \phi_e)/T = \frac{1}{2}\phi^2 + \phi_j(\ln\phi_j - 1) + \phi_e(\ln\phi_e - 1) + \phi_j(\epsilon_j/T - \ln a_f) + \phi_e\epsilon_e/T - \frac{f}{2}\phi_j\ln\phi - \frac{1}{2}\phi_e\ln\phi \tag{2}$$

The first term is the excluded volume of the chains, the next four terms represent the free energy of an "ideal gas" of junctions and ends, and the last two terms are the increase in the free energy of this "ideal gas" due to the fact that the junctions and the ends are constrained to a network. Each junction confines $f/2$ monomers to the same point in space which increases the free energy by $\frac{f}{2}\phi_j\mu_\phi$ where $\mu_\phi \simeq T\ln\phi$ is the chemical potential of a "gas" of monomers. Similarly, last term reflects the reduction in the entropy of a "gas" of ends due to the fact that two ends are constrained to lie on the same chain. Because each junction requires one cross-link molecule and each end uses up one end cap molecule, the *total* free energy of the system is $F^{\text{tot}}(\phi, \phi_j, c) = F(\phi, \phi_j, \phi_e) + F_c(c - \phi_j) + F_e(\rho - \phi_e)$, where $F_c(c - \phi_j)$ and $F_e(\rho - \phi_e)$ are the free energies of the unbound cross-links and ends, respectively. We take these both to be ideal solutions: $F_e(\psi) = F_c(\psi) = T\psi(\ln\psi - 1)$. The total free energy $F^{\text{tot}}(\phi, \phi_j, \phi_e, c, \rho)$ is minimized with respect to ϕ_j and ϕ_e to find the equilibrium end and junction density as a function of $\phi, \epsilon_j, \epsilon_e, c, \rho$ and T. This predicts that the junction and end densities vary with the monomer, cross-link and end-cap densities as

$$\phi_e = \rho e^{-\epsilon_e/T}\phi^{1/2}/\left(1 + e^{-\epsilon_e/T}\phi^{1/2}\right) \qquad \phi_j = ca_f e^{-\epsilon_j/T}\phi^{f/2}/\left(1 + a_f e^{-\epsilon_j/T}\phi^{f/2}\right) \tag{3}$$
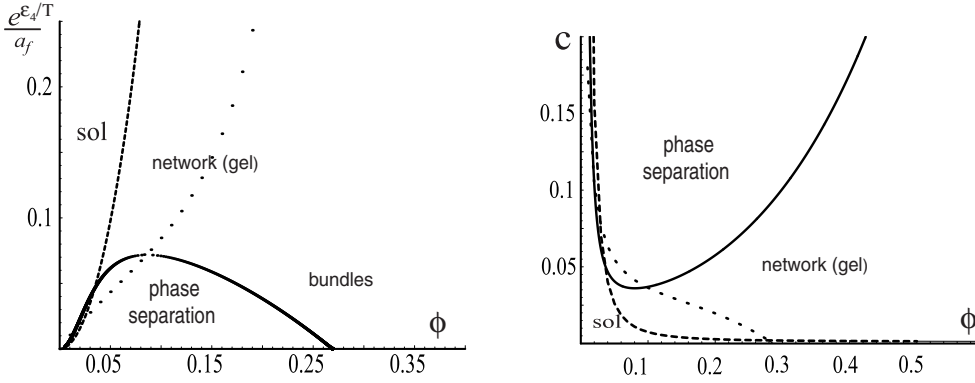
Fig. 1 – (a) The monomer concentration-temperature, $\left(\phi, e^{\epsilon_4/T}/a_f\right)$, plane of the phase diagram for strong, four-fold junctions for $\epsilon_j, \epsilon_e < 0$ and $\epsilon_4/\epsilon_e = 1$; $c = 0.05, \rho = 0.005$. The thick line shows the spinodal of the junctions-ends transition. The dashed line is the percolation line to the right of which a connected network is formed. The bundles appear to the right of the dotted line; $a_f/q = 1$. (b) Monomer/crosslink concentration, (ϕ, c), section of the phase diagram for $a_f e^{\epsilon_4/T} = 0.015$, $|\epsilon_e/\epsilon_4| = 10/3, \rho = 0.005$. The upper line delineates the region of the phase separation. The lower, dashed, curve is the percolation line, above which a connected network is formed. Bundles are predicted to appear to the right of the dotted line.

It is important to note that the density of junctions ϕ_j behaves rather differently for strong ($\epsilon_j < 0$) and weak ($\epsilon_j > 0$) cross-linking. In the limit of very strong junctions ($\epsilon_j < 0, |\frac{\epsilon_j}{T}| \gg 1$), the junction density saturates to a value equal to the cross-link concentration, c.

This means, that in this limit (i) almost all cross-link molecules are found in the junctions (ii) the junctions persist at low temperatures. In the opposite limit of weak junctions, $\phi_j \simeq c a_f e^{-\epsilon_j/T}\phi^{f/2} \ll c$ which means that (i) most of the cross-link molecules are found in solution and not in junctions (ii) at low temperatures, the number of thermally generated junctions tends to zero. Also, it follows from Eq.(3) that the condition of sparse junctions, used in the derivation of Eq.(1) is always satisfied as long as $c \ll \phi$.

Substituting the expression of Eq.(3) for ϕ_j back into the free energy F, gives:

$$F^{\text{tot}}(\phi, c) = \frac{1}{2}\phi^2 + c\left(\ln c - 1\right) + \rho\left(\ln \rho - 1\right) - c\ln(1 + a_f e^{-\epsilon_j/T}\phi^{f/2}) - \rho\ln\left(1 + e^{-\epsilon_e/T}\phi^{1/2}\right) \quad (4)$$

The last two terms are the free energy reduction due to the presence of thermally generated ends and junctions. Although both these terms represent negative contributions to the free energy, the term associated with the ends is thermodynamically equivalent to a *repulsion* while the term associated with the junctions induces an effective thermodynamic *attraction* between the monomers. This can be seen by considering the osmotic pressure, $\Pi = \rho\frac{\partial F}{\partial \rho} + \phi\frac{\partial F}{\partial \phi} + c\frac{\partial F}{\partial c} - F$, to which the junctions give a *negative* contribution, $-\frac{f}{2}c a_f e^{-\epsilon_j/T}\phi^{f/2}/(1 + a_f e^{-\epsilon_j/T}\phi^{f/2})$ while the ends give a *positive* contribution $+\frac{1}{2}\rho e^{-\epsilon_e/T}\phi^{1/2}/(1 + e^{-\epsilon_e/T}\phi^{1/2})$.

Phase Separation and Gelation: If the density of cross link molecules is sufficiently high, or the temperature is sufficiently low, the junction induced attraction can be strong enough to drive a phase separation between a dense, junction rich, network and a dilute phase consisting either of weakly branched chains or a very sparse network.

For thermodynamic stability, the free energy $F^{\text{tot}}(\phi, c, \rho)$ must be convex with respect to all the thermodynamic variables ϕ, c and ρ. Technically, this requires that the matrix of

second derivatives of $F^{\text{tot}}(\phi, c, \rho)$ is positive definite (i.e., has three positive eigenvalues). This condition defines the spinodal surface of the phase separation in the phase space of the system, and the critical density of cross-links, $c_{\text{s}}(\phi, \rho, T)$, as a function of the end cap concentration, the monomer concentration and the temperature, is given by:

$$c_{\text{s}}(\phi, \rho, T) = \frac{4}{f(f-2)\,a_f} \left(\frac{\phi^{(4-f)/2} e^{\epsilon_j/T}}{1-\phi} + \frac{1}{4}\rho \frac{\phi^{(1-f)/2} e^{(\epsilon_j-\epsilon_e)/T}}{1+\phi^{1/2} e^{-\epsilon_e/T}} \right) \left(1 + a_f e^{-\epsilon_j/T} \phi^{f/2} \right) \quad (5)$$

In the (c, ϕ) plane, the system is stable for cross-link densities $c < c_{\text{s}}(\phi)$, while for $c > c_{\text{s}}(\phi)$ the system separates into a dense network with many junctions, in equilibrium with a dilute phase. Similarly, in the (T, ϕ) plane, at a given cross-link density c, the system is unstable for a certain range of monomer densities ϕ as shown in Fig. 1. The dilute phase can be either a very sparse network or consist of disjointed, weakly branched clusters. The dense phase is usually a connected network, as discussed below. The thermodynamic behavior is rather different for weak and for strong cross-links. In the case of weak cross-links ($\epsilon_j > 0$, $\epsilon_j/T \gg 1$) the junction-induced attraction is strong enough to drive the phase separation only for three-fold junctions, $f = 3$. In addition, the phase transition in the case of weak junctions is *reentrant* because the number of thermally generated junctions tends to zero as the temperature is lowered as follows from Eq.(3). In contrast, in the case of strong junctions ($\epsilon_j < 0$), the phase separation occurs for junctions of any functionality as follows from Eq.(5); the transition is not reentrant because the number of junctions *increases* with decreasing temperature, as follows from Eq.(3). The predicted phase transition is *entropic in origin*. In the dense phase, the entropy of the large number of the formed junctions compensates for the loss of the translational entropy of the monomers.

For sparse junctions, in the mean field approximation [2, 12, 29], a connected network spanning the entire system is formed when $f(f-2)\phi_j = \phi_e$. This gelation or percolation transition, is a continuous, purely *topological* transition that has no thermodynamic signature. Thus, a connected network spanning the entire system is formed when the cross link concentration exceeds the value

$$c_{\text{perc}} = \rho/(f(f-2)a_f)\phi^{(1-f)/2} e^{(\epsilon_j-\epsilon_e)/T} \left(1 + e^{-\epsilon_j/T} \phi^{1/2} \right) / \left(1 + a_f e^{-\epsilon_e/T} \phi^{f/2} \right)$$

This allows one to predict the gelation line in the phase diagram of the system, as shown in Fig. 1.

In vitro experiments on solutions of rigid actin filaments, cross-linked with α-actinin and in presence of the capping protein gelsolin, found that the system undergoes a continuous, non-thermodynamic transition from an entangled network of branched clusters to a "microgel" [4] that results in a sharp increase in viscosity, and can be interpreted in terms of percolation. At lower temperatures, it was found that the system undergoes a first-order phase separation into a dilute solution of short chains in equilibrium with a dense network that consists mostly of bundles of actin filaments, tightly bound by cross-links. These observations are consistent with the phase diagram of Fig. 1.

Bundles: The formation of bundles can be understood in terms of the entropy of rigid chains (rods) and cross links that join two rods or four monomers, $f = 4$. In the bundle phase, the rotational and translational entropy of the rods is lower than in the isotropic, network phase. However, the entropy of positioning the junctions on the parallel "tracks" formed by the rods found in bundles is higher than in the network, where junction positions are confined to the intersections between the rods. It turns out that this effect favors the formation of bundles at low temperatures. As a first step, we estimate that the transition from an isotropic network to bundles takes place when their free energies become equal. Assuming that the energy of

the ends is large and negative, so that all the end cap molecules are bound to chain ends, the free energy of the isotropic phase (neglecting a term that depends on the number of end caps and is the same in both phases) is given by Eq.4:

$$F_i/T \simeq \frac{1}{2}\phi^2 + c(\ln c - 1) - c\ln\left(1 + a_f e^{-\epsilon_j/T}\phi^2\right) + \rho\left(\ln\left(\rho/\phi^{1/2}\right) - 1\right)$$

We describe the bundle state as a collection of N_b bundles of m rods of length L. The N_j junctions formed by the cross links can be placed between any two adjacent rods. If the number of nearest neighbor rods in a bundle is $2q$, there are $N_b(qm - qm^{1/2}/2)$ available one-dimensional "tracks" for the junctions, because the rods at the perimeter of a bundle have half as many neighbors as the interior rods; the number of perimeter rods $\sim m^{1/2}$ for large bundles. The junction entropy is then $\sim \frac{1}{N_j!}\left(qN_bLm\left[1 - 1/\left(2m^{1/2}\right)\right]\right)^{N_j}$. Noting that N_bLm is the total number of monomers in the system and recalling that the energy of a junction is ϵ_j, we find for the free energy of the bundle phase

$$F_b/T \simeq \phi_j\left(\ln\phi_j - 1\right) - \phi_j\ln\left(q\phi\left(1 - 1/\left(2m^{1/2}\right)\right)\right) + \phi_j\epsilon_j/T + (c - \phi_j)\left(\ln\left(c - \phi_j\right) - 1\right)$$

where the last term accounts for the translational entropy of the free cross-links in the solution. Note that the junction-related part of the bundle state is *lower* than the corresponding part of the free energy of an isotropic network, eq.(2), because the entropic cost of confining a junction to lie on a track between two parallel rods is $-\ln\left(q\phi\left(1 - 1/\left(2m^{1/2}\right)\right)\right)$ and is lower than the corresponding cost of confinement to an intersection of two rods in a three dimensional network, $-2\ln\phi$. Minimizing the free energy as a function of the junction density, ϕ_j, gives for the junction-related part of the free energy, $F_b/T \simeq c(\ln c - 1) - c\ln\left(1 + e^{-\epsilon_j/T}q\phi\left(1 - 1/\left(2m^{1/2}\right)\right)\right)$.

In addition to the configurational entropy of cross-link distribution among the filaments, the free energy of the bundled states includes the following contributions: (i) the translational entropy of the bundles $\frac{\rho}{m}\left(\ln\frac{\rho}{m\phi^{1/2}} - 1\right)$ and (ii) the *reduction* in the rotational entropy of the bundles relative to the isotropic phase, $\rho\left(1 - \frac{1}{m}\right)\ln 4\pi$ [16,17,20] and (iii) the excluded volume repulsion between the bundles, $\frac{1}{2}v\left(\phi/(mL)\right)^2$ where $v \simeq m^{1/2}L^2$ [16], because the diameter of the bundle of m rods is proportional to $m^{1/2}$. Without (i) and (ii), that balance the increase of the configurational cross-link entropy in the bundle phase, the bundles would be always preferred thermodynamically. Although the free energy of the bundle state can have a minimum at finite values of m, it turns out that this region is small [32], and for a first estimate we assume that the bundle state consists of one macroscopic bundle. In the limit of $m \to \infty$, $F_b/T \simeq c(\ln c - 1) - c\ln\left(1 + e^{-\epsilon_j/T}\phi\right) + \rho\ln 4\pi$. The transition to bundles, therefore, takes place when $F_b < F_i$, that is $e^{\epsilon_j/T}/a_f < \phi\frac{qe^A/a_f - \phi}{1 - e^A}$ where $Ac = \frac{1}{2}\phi^2 - \rho\ln 4\pi$, as shown in Fig.1. The location of the network to bundle transition line in the phase diagram is sensitive to the value of the parameter q/a_f, where a_f reflects the number of internal configurations of a cross-link in the isotropic network relative to parallel bundles; increasing q/a_f decreases the threshold for bundle formation. The parameter a_f, as well as the energies ϵ_e and ϵ_j can be estimated experimentally from the number of bound cross-links, and the length distribution of chain segments among them. However, when comparing with the experimental results of [4], one should bear in mind, that for long chains, the formation of the bundles might be kinetically inhibited and may not be experimentally observable.

$$* * *$$

REFERENCES

[1]   M. Albers *et al.*, *Molecular Biology of the Cell*, Garland Publishing, New York, 1994
[2]   P. J. Flory, Principles of Polymer Chemistry, Cornell University Press, 1981.
[3]   D. Eizenberg, W. Kaufmann, The structure and Properties of Water, Oxford University Press, 1969
[4]   M. Tempel, G. Isenberg, E. Sackmann, Phys. Rev. E, 54, 1802 (1996).
[5]   T. Tlusty, S.A. Safran, Science, 290, 1328 (2000)
[6]   J.C. Wheeler, P. Pfeuty, Phys. Rev. A, 24, 1050 (1981)
[7]   F. Lequeux, K. Elleuch, P. Pfeuty, J. Phys I, 5, 465 (1995)
[8]   A.N. Semenov, M. Rubinstein, Macromolecules, 31, 1373 (1988)
[9]   S.K. Kumar, A. Z. Panagiotopoulos, Phys. Rev. Lett., 82, 5060 (1999) *and references therein*
[10] H. Takeshita *et.al.* Macromolecules, 34 , 7894 (2001)   *and referneces therein*
[11] J. T. Kindt, J. Phys. Chem. B, 106, 8223 (2002)
[12] T.C. Lubensky, J. Isaacson, Phys. Rev. Lett. 41, 829 (1978); T.C. Lubensky, J. Isaacson, Phys. Rev. A 20, 2130-2146 (1979)
[13] A.B. Harris *et al.*, Phys. Rev. Lett., 35, 327 (1975); R. Kikuchi, J. Chem. Phys, 53, 2713 (1970); A. Coniglio, Phys. Rev. B, 13, 2194 (1976); K.K. Murata, J. Phys. A, 12, 81 (1979)
[14] F. Tanaka, Physica A, 257, 245 (1998), F. Tanaka, Macromolecules, 31, 384 (1998)
[15] M. Filali *et. al.*, J. Phys. Chem. B. 105, 10528 (2001)
[16] L. Onsager, Ann. N. Y. Acad. Sci., 51, 627 (1949)
[17] P.-G. DeGennes, J. Prost, The Physics of Liquid Crystals, Oxford University Press, 1995
[18] A. N. Semenov, I. A. Nyrkova, M. E. Cates, Macromolecules, 28, 7879 (1995)
[19] T. Drye, M.E. Cates, J. Chem. Phys. 96 (2), 1367 (1992); T. Tlusty T, S.A. Safran, R. Strey, Phys. Rev. Lett., 84, 1244 (2000)
[20] I. Borukhov et. al. Phys. Rev. Lett., 87, 158101 (2001)
[21] J. C. Butler, T. Angelini, J. X. Tang, G. C. L. Wong, Phys. Rev. Lett., 91, 028301 (2003) *and references therein*
[22] V. A. Bloomfield, Biopolymers, 44, 269 (1997)
[23] T. T. Nguyen, I. Rouzina, B. I. Shklovskii, J Chem. Phys. 112, 2562 (2000)
[24] A. Berheim-Groswasser *et al.*, Langmuir, 15: 5448 (1999); A. Berheim-Groswasser *et al.*, Langmuir, 16, 4131 (2000)
[25] R. Strey *et al.*, J. Chem. Phys, 105, 1175 (1996); F. Lichterfeld *et al*, J. Phys. Chem., 90, 5762 (1986) *and references therein*
[26] A. Khatory *et al.*, Langmuir, 9, 933 (1993); E. Buhler *et al.*, J. Phys II, 5, 765 (1995)
[27] T. Tanaka *et al.*, Phys. Rev. Lett, 42, 1556 (1979); T. Miura *et al.*, Phys. Rev. E, 54, 6596 (1996); A. Moussaid *et. al.*, J. Phys II, 1, 637 (1991) *and references therein*
[28] G. Cristobal *et al.*, Physica A, 268, 50 (1999)
[29] A.G. Zilman and S.A. Safran, Phys. Rev. E. 66, 051107 (2002)
[30] A. Zilman, J. Kieffer, F. Molino, G. Porte, S. Safran, Phys. Rev. Lett., 91, 015901,(2003)
[31] I. Borukhov, K. C. Lee, R. F. Bruinsma, W. M. Gelbart *et. al.*, J Chem. Phys., 117, 462 (2002)
[32] A. Zilman, S. Safran, *to be published*